

SEQUENCE LISTING

(1). GENERAL INFORMATION:

- (i) APPLICANT(S): Kaufman, Randal J.
Wasley, Louise
- (ii) TITLE OF INVENTION: Method of Increasing Yield of
Mature Proteins
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: United States of America
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage
 - (B) COMPUTER: IBM PS/2
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: not yet available
 - (B) FILING DATE: 26 November 1990
 - (C) CLASSIFICATION: not yet available
- (vii) PRIOR APPLICATION DATA: not applicable
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Ellen J. Kapinos, Esquire
 - (B) REGISTRATION NUMBER: 32,245
 - (C) REFERENCE/DOCKET NUMBER: GI 5181
- (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 876-1170
(B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2385 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) Topology: unknown

(ii) MOLECULE TYPE: partial human genomic DNA

(A) DESCRIPTION: sequence encoding furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION: A.M.W. van den Ouweland et al,
Nucl. Acids. Res., 18:664 (1990)

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:1

ATG GAG CTC AGG CCC TGG TTC	21
Met Glu Leu Arg Pro Trp Leu	
1 5	
CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA	60
Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu	
10 15 20	
GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG	99
Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr	
25 30	
TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC	138
Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn	
35 40 45	
AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG	177
Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln	
50 55	
ATC TTC GGG GAC TAT TAC CAC TTC TGG CAT CGA GGA GTG	216
Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val	
60 65 70	

ACG	AAG	CGG	TCC	CTG	TCG	CCT	CAC	CGC	CCG	CGG	CAC	AGC	255
Thr	Lys	Arg	Ser	Leu	Ser	Pro	His	Arg	Pro	Arg	His	Ser	
		75					80					85	
CGG	CTG	CAG	AGG	GAG	CCT	CAA	GTA	CAG	TGG	CTG	GAA	CAG	294
Arg	Leu	Gln	Arg	Glu	Pro	Gln	Val	Gln	Trp	Leu	Glu	Gln	
				90					95				
CAG	GTG	GCA	AAG	CGA	CGG	ACT	AAA	CGG	GAC	GTG	TAC	CAG	333
Gln	Val	Ala	Lys	Arg	Arg	Thr	Lys	Arg	Asp	Val	Tyr	Gln	
	100					105					110		
GAG	CCC	ACA	GAC	CCC	AAG	TTT	CCT	CAG	CAG	TGG	TAC	CTG	372
Glu	Pro	Thr	Asp	Pro	Lys	Phe	Pro	Gln	Gln	Trp	Tyr	Leu	
			115					120					
TCT	GGT	GTC	ACT	CAG	CGG	GAC	CTG	AAT	GTG	AAG	GCG	GCC	411
Ser	Gly	Val	Thr	Gln	Arg	Asp	Leu	Asn	Val	Lys	Ala	Ala	
125					130					135			
TGG	GCG	CAG	GGC	TAC	ACA	GGG	CAC	GGC	ATT	CTG	GTC	TCC	450
Trp	Ala	Gln	Gly	Tyr	Thr	Gly	His	Gly	Ile	Val	Val	Ser	
		140					145					150	
ATT	CTG	GAC	GAT	GGC	ATC	GAG	AAG	AAC	CAC	CCC	GAC	TTG	489
Ile	Leu	Asp	Asp	Gly	Ile	Glu	Lys	Asn	His	Pro	Asp	Leu	
				155					160				
GCA	GGC	AAT	TAT	GAT	CCT	GGG	GCC	AGT	TTT	CAT	GTC	AAT	528
Ala	Gly	Asn	Tyr	Asp	Pro	Gly	Ala	Ser	Phe	Asp	Val	Asn	
	165					170					175		
GAC	CAG	GAC	CCT	GAC	CCC	CAG	CCT	CGG	TAC	ACA	CAG	ATG	567
Asp	Gln	Asp	Pro	Asp	Pro	Gln	Pro	Arg	Tyr	Thr	Gln	Met	
			180					185					
AAT	GAC	AAC	AGG	CAC	GGC	ACA	CGG	TGT	GCG	GGG	GAA	GTG	606
Asn	Asp	Asn	Arg	His	Gly	Thr	Arg	Cys	Ala	Gly	Glu	Val	
190					195					200			
GCT	GCC	GTG	GCC	AAC	AAC	CGT	GTC	TGT	GGT	GTA	GGT	GTG	645
Ala	Ala	Val	Ala	Asn	Asn	Gly	Val	Cys	Gly	Val	Gly	Val	
		205					210					215	
GCC	TAC	AAC	GCC	CGC	ATT	GGA	GGG	GTC	CGC	ATG	CTG	GAT	684
Ala	Tyr	Asn	Ala	Arg	Ile	Gly	Gly	Val	Arg	Met	Leu	Asp	
				220					225				
GGC	GAG	GTG	ACA	GAT	GCA	GTG	GAG	GCA	CGC	TCG	CTG	GGC	723
Gly	Glu	Val	Thr	Asp	Ala	Val	Glu	Ala	Arg	Ser	Leu	Gly	
	230					235					240		
CTG	AAC	CCC	AAC	CAC	ATC	CAC	ATC	TAC	AGT	GCC	AGC	TGG	762

Arg	Leu	Gln	Arg	Glu	Pro	Gln	Val	Gln	Trp	Leu	Glu	Gln
				90					95			
Gln	Val	Ala	Lys	Arg	Arg	Thr	Lys	Arg	Asp	Val	Tyr	Gln
	100					105					110	
Glu	Pro	Thr	Asp	Pro	Lys	Phe	Pro	Gln	Gln	Trp	Tyr	Leu
			115					120				
Ser	Gly	Val	Thr	Gln	Arg	Asp	Leu	Asn	Val	Lys	Ala	Ala
125					130					135		
Trp	Ala	Gln	Gly	Tyr	Thr	Gly	His	Gly	Ile	Val	Val	Ser
		140					145					150
Ile	Leu	Asp	Asp	Gly	Ile	Glu	Lys	Asn	His	Pro	Asp	Leu
				155					160			
Ala	Gly	Asn	Tyr	Asp	Pro	Gly	Ala	Ser	Phe	Asp	Val	Asn
	165					170					175	
Asp	Gln	Asp	Pro	Asp	Pro	Gln	Pro	Arg	Tyr	Thr	Gln	Met
			180					185				
Asn	Asp	Asn	Arg	His	Gly	Thr	Arg	Cys	Ala	Gly	Glu	Val
190					195					200		
Ala	Ala	Val	Ala	Asn	Asn	Gly	Val	Cys	Gly	Val	Gly	Val
		205					210					215
Ala	Tyr	Asn	Ala	Arg	Ile	Gly	Gly	Val	Arg	Met	Leu	Asp
				220					225			
Gly	Glu	Val	Thr	Asp	Ala	Val	Glu	Ala	Arg	Ser	Leu	Gly
	230					235					240	
Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp
			245					250				
Gly	Pro	Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala
255					260					265		
Arg	Leu	Ala	Glu	Glu	Ala	Phe	Phe	Arg	Gly	Val	Ser	Gln
		270					275					280
Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	Phe	Val	Trp	Ala	Ser
				285					290			
Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	Cys	Asp
	295					300					305	
Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser
			310					315				

Leu	Asn	Pro	Asn	His	Ile	His	Ile	Tyr	Ser	Ala	Ser	Trp	
			245					250					
GGC	CCC	GAG	GAT	GAC	GGC	AAG	ACA	GTG	GAT	GGG	CCA	GCC	801
Gly	Pro	Glu	Asp	Asp	Gly	Lys	Thr	Val	Asp	Gly	Pro	Ala	
255					260					265			
CGG	CTC	GCC	GAG	GAG	GCC	TTC	TTC	CGT	GGG	CTT	AGC	CAG	840
Arg	Leu	Ala	Glu	Glu	Ala	Phe	Phe	Arg	Gly	Val	Ser	Gln	
		270					275					280	
GGC	CGA	GGG	GGG	CTG	GGC	TCC	ATC	TTT	GTC	TGG	GCC	TCG	879
Gly	Arg	Gly	Gly	Leu	Gly	Ser	Ile	Phe	Val	Trp	Ala	Ser	
				285					290				
GGG	AAC	GGG	GGG	CGG	GAA	CAT	GAC	AGC	TGC	AAC	TGC	GAC	918
Gly	Asn	Gly	Gly	Arg	Glu	His	Asp	Ser	Cys	Asn	Cys	Asp	
	295					300					305		
GGC	TAC	ACC	AAC	AGT	ATC	TAC	ACG	CTG	TCC	ATC	AGC	AGC	957
Gly	Tyr	Thr	Asn	Ser	Ile	Tyr	Thr	Leu	Ser	Ile	Ser	Ser	
			310					315					
GCC	ACG	CAG	TTT	GGC	AAC	GTG	CCG	TGG	TAC	AGC	GAG	GCC	996
Ala	Thr	Gln	Phe	Gly	Asn	Val	Pro	Trp	Tyr	Ser	Glu	Ala	
320					325					330			
TGC	TCG	TCC	ACA	CTG	GCC	ACG	ACC	TAC	AGC	AGT	GGC	AAC	1035
Cys	Ser	Ser	Thr	Leu	Ala	Thr	Thr	Tyr	Ser	Ser	Gly	Asn	
		335					340					345	
CAG	AAT	GAG	AAG	CAG	ATC	GTG	ACG	ACT	GAC	TTG	CGG	CAG	1074
Gln	Asn	Glu	Lys	Gln	Ile	Val	Thr	Thr	Asp	Leu	Arg	Gln	
				350					355				
AAG	TGC	ACG	GAG	TCT	CAC	ACG	GGC	ACC	TCA	GCC	TCT	GCC	1113
Lys	Cys	Thr	Glu	Ser	His	Thr	Gly	Thr	Ser	Ala	Ser	Ala	
	360					365					370		
CCC	TTA	GCA	GCC	GGC	ATC	ATT	GCT	CTC	ACC	CTG	GAG	GCC	1152
Pro	Leu	Ala	Ala	Gly	Ile	Ile	Ala	Leu	Thr	Leu	Glu	Ala	
			375					380					
AAT	AAG	AAC	CTC	ACA	TGG	CGG	GAC	ATG	CAA	CAC	CTG	GTG	1191
Asn	Lys	Asn	Leu	Thr	Trp	Arg	Asp	Met	Gln	His	Leu	Val	
385					390					395			
GTA	CAG	ACC	TCG	AAG	CCA	GCC	CAC	CTC	AAT	GCC	AAC	GAC	1230
Val	Gln	Thr	Ser	Lys	Pro	Ala	His	Leu	Asn	Ala	Asn	Asp	
		400					405					410	
TGG	GCC	ACC	AAT	GGT	GTG	GGG	CGG	AAA	GTG	AGC	CAC	TCA	1269
Trp	Ala	Thr	Asn	Gly	Val	Gly	Arg	Lys	Val	Ser	His	Ser	
				415					420				

TAT	GGC	TAC	GGG	CTT	TTC	GAC	GCA	GGC	GCC	ATG	GTG	GCC	1308
Tyr	Gly	Tyr	Gly	Leu	Leu	Asp	Ala	Gly	Ala	Met	Val	Ala	
	425					430					435		
CTG	GCC	CAG	AAT	TGG	ACC	ACA	GTC	GCC	CCC	CAG	CGG	AAG	1347
Leu	Ala	Gln	Asn	Trp	Thr	Thr	Val	Ala	Pro	Gln	Arg	Lys	
		440						445					
TGC	ATC	ATC	GAC	ATC	CTC	ACC	GAG	CCC	AAA	GAC	ATC	GGG	1386
Cys	Ile	Ile	Asp	Ile	Leu	Thr	Glu	Pro	Lys	Asp	Ile	Gly	
450					455					460			
AAA	CGG	CTC	GAC	CTC	CGG	AAC	ACC	GTG	ACC	GCG	TCC	CTG	1425
Lys	Arg	Leu	Glu	Val	Arg	Lys	Thr	Val	Thr	Ala	Cys	Leu	
	465					470						475	
GGC	GAG	CCC	AAC	CAC	ATC	ACT	CGG	CTG	GAG	CAC	GCT	CAG	1464
Gly	Glu	Pro	Asn	His	Ile	Thr	Arg	Leu	Glu	His	Ala	Gln	
				480					485				
GCG	CGG	CTC	ACC	CTG	TCC	TAT	AAT	CGC	CGT	GGC	GAC	CTG	1503
Ala	Arg	Leu	Thr	Leu	Ser	Tyr	Asn	Arg	Arg	Gly	Asp	Leu	
	490					495					500		
GCC	ATC	CAC	CTG	GTC	AGC	CCC	ATG	GGC	ACC	CGC	TCC	ACC	1542
Ala	Ile	His	Leu	Val	Ser	Pro	Met	Gly	Thr	Arg	Ser	Thr	
			505					510					
CTG	CTG	GCA	GCC	AGG	CCA	CAT	GAC	TAC	TCC	GCA	GAT	GGG	1581
Leu	Leu	Ala	Ala	Arg	Pro	His	Asp	Tyr	Ser	Ala	Asp	Gly	
515					520					525			
TTT	AAT	GAC	TGG	GCC	TTC	ATG	ACA	ACT	CAT	TCC	TGG	GAT	1620
Phe	Asn	Asp	Trp	Ala	Phe	Met	Thr	Thr	His	Ser	Trp	Asp	
		530				535						540	
GAC	GAT	CCC	TCT	GGG	GAG	TGG	GTC	CTA	GAG	ATT	GAA	AAC	1659
Glu	Asp	Pro	Ser	Gly	Glu	Trp	Val	Leu	Glu	Ile	Glu	Asn	
				545					550				
ACC	AGC	GAA	GCC	AAC	AAC	TAT	GGG	ACG	CTG	ACC	AAC	TCC	1698
Thr	Ser	Glu	Ala	Asn	Asn	Tyr	Gly	Thr	Leu	Thr	Lys	Phe	
	555					560					565		
ACC	CTC	GTA	CTC	TAT	GGC	ACC	GCC	CCT	GAC	GGG	CTC	CCC	1737
Thr	Leu	Val	Leu	Tyr	Gly	Thr	Ala	Pro	Glu	Gly	Leu	Pro	
			570					575					
GTA	CCT	CCA	GAA	AGC	AGT	GGC	TGC	AAG	ACC	CTC	ACG	TCC	1776
Val	Pro	Pro	Glu	Ser	Ser	Gly	Cys	Lys	Thr	Leu	Thr	Ser	
580					585					590			
AGT	CAG	GCC	TGT	GTG	GTG	TGC	GAG	GAA	GGC	TTC	TCC	CTC	1815
Ser	Gln	Ala	Cys	Val	Val	Cys	Glu	Glu	Gly	Phe	Ser	Leu	

595					600					605				
CAC	CAG	AAG	AGC	TGT	GTC	CAG	CAC	TGC	CCT	CCA	GGC	TTC	1854	
His	Gln	Lys	Ser	Cys	Val	Gln	Asn	Cys	Pro	Pro	Gly	Phe		
				610					615					
GCC	CCC	CAA	GTC	CTC	GAT	ACG	CAC	TAT	AGC	ACC	GAG	AAT	1893	
Ala	Pro	Gln	Val	Leu	Asp	Thr	Asn	Tyr	Ser	Thr	Glu	Asn		
	620					625					630			
GAC	GTG	GAG	ACC	ATC	CGG	GCC	AGC	GTC	TGC	GCC	CCC	TGC	1932	
Asp	Val	Glu	Thr	Ile	Arg	Ala	Ser	Val	Cys	Ala	Pro	Cys		
			635					640						
CAC	GCC	TCA	TGT	GCC	ACA	TGC	CAG	GGG	CCG	GCC	CTG	ACA	1971	
His	Ala	Ser	Cys	Ala	Thr	Cys	Gln	Gly	Pro	Ala	Leu	Thr		
	645				650					655				
GAC	TGC	CTC	AGC	TGC	CCC	AGC	CAC	GCC	TCC	TTG	GAC	CCT	2010	
Asp	Cys	Leu	Ser	Cys	Pro	Ser	His	Ala	Ser	Leu	Asp	Pro		
		660					665					670		
GTG	GAG	CAG	ACT	TGC	TCC	CGG	CAA	AGC	CAG	AGC	AGC	CGA	2049	
Val	Glu	Gln	Thr	Cys	Ser	Arg	Gln	Ser	Gln	Ser	Ser	Arg		
				675					680					
GAG	TCC	CCG	CCA	CAG	CAG	CAG	CCA	CCT	CGG	CTG	CCC	CCG	2088	
Glu	Ser	Pro	Pro	Gln	Gln	Gln	Pro	Pro	Arg	Leu	Pro	Pro		
	685					690					695			
GAG	GTG	GAG	GCG	GGG	CAA	CGG	CTG	CGG	GCA	GGG	CTG	CTG	2127	
Glu	Val	Glu	Ala	Gly	Gln	Arg	Leu	Arg	Ala	Gly	Leu	Leu		
			700					705						
CCC	TCA	CAC	CTG	CCT	GAG	GTG	GTG	GCC	GGC	CTC	AGC	TGC	2166	
Pro	Ser	His	Leu	Pro	Glu	Val	Val	Ala	Gly	Leu	Ser	Cys		
					715					720				
GCC	TTC	ATC	GTG	CTG	GTC	TTC	GTC	ACT	GTC	TTC	CTG	CTC	2205	
Ala	Phe	Ile	Val	Leu	Val	Phe	Val	Thr	Val	Phe	Leu	Val		
		725					730					735		
CTG	CAG	CTG	CGC	TCT	GGC	TTT	AGT	TTT	CGG	GGG	GTG	AAG	2244	
Leu	Gln	Leu	Arg	Ser	Gly	Phe	Ser	Phe	Arg	Gly	Val	Lys		
				740					745					
GTG	TAC	ACC	ATG	GAC	CGT	GGC	CTC	ATC	TCC	TAC	AAG	GGG	2283	
Val	Tyr	Thr	Met	Asp	Arg	Gly	Leu	Ile	Ser	Tyr	Lys	Gly		
	750					755					760			
CTG	CCC	CCT	GAA	GCC	TGG	CAG	GAG	GAG	TGC	CCG	TCT	GAC	2322	
Leu	Pro	Pro	Glu	Ala	Trp	Gln	Glu	Glu	Cys	Pro	Ser	Asp		
			765					770						

TCA GAA GAG GAC GAG GGC CGG GGC GAG AGG ACC GCC TTT 2361
 Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
 775 780 785

ATC AAA GAC CAG AGC GCC CTC TGA 2385
 Ile Lys Asp Gln Ser Ala Leu End
 790

(3) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 amino acids

(B) TYPE: amino acids

(C) STRANDEDNESS: single

(D) Topology: unknown

(ii) MOLECULE TYPE: furin

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) PUBLICATION INFORMATION: A.M.W. van den Ouweland et al,
Nucl. Acids. Res., 18:664 (1990)

(vi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Met Glu Leu Arg Pro Trp Leu
 1 5

Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
 10 15 20

Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
 25 30

Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
 35 40 45

Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln
 50 55

Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val
 60 65 70

Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser
 75 80 85

Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala
 320 325 330
 Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn
 335 340 345
 Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln
 350 355
 Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala
 360 365 370
 Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
 375 380
 Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val
 385 390 395
 Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp
 400 405 410
 Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser
 415 420
 Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala
 425 430 435
 Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys
 440 445
 Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly
 450 455 460
 Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
 465 470 475
 Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
 480 485
 Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
 490 495 500
 Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
 505 510
 Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
 515 520 525
 Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
 530 535 540
 Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
 545 550

Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
 555 560 565
 Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
 570 575
 Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
 580 585 590
 Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
 595 600 605
 His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
 610 615
 Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
 620 625 630
 Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
 635 640
 His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
 645 650 655
 Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
 660 665 670
 Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
 675 680
 Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
 685 690 695
 Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
 700 705
 Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
 710 715 720
 Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
 725 730 735
 Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
 740 745
 Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
 750 755 760
 Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
 765 770
 Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
 775 780 785

Ile Lys Asp Gln Ser Ala Leu End
790